

1 ATGCTGTTCCGCGCCCCGGGGCCGGTACGGGGCAGGGGCTGGGGCGGGCGCGGAGGCT 60
 1 M L F R A R G P V R G R G W G R P A E A 20
 61 CCCCCCGCGGGGCTCGCCGCCCTGGAGCCCCGCTGGATTGCTGCTGGGCGCTCGCC 120
 21 P R R G R S P P W S P A W I C C W A L A 40
 121 GGCTGCCAGGCGGCTGGGCTGGGGACCTGCCCTCCTCCTCCAGCCGCGCGCTTCCTCCT 180
 41 G C Q A A W A G D L P S S S S R P L P P 60
 181 TGCCAGGAGAAAGATTATCACTTTGAATATACGGAATGTGATAGCAGTGGCTCCAGGTGG 240
 61 C Q E K D Y H F E Y T E C D S S G S R W 80
 241 AGAGTTGCCATTCCAAATTCTGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGC 300
 81 R V A I P N S A V D C S G L P D P V R G 100
 301 AAAGAATGCACTTTCTCCTGTGCTTCTGGACAGTATCTAGAAATGAAGAACCAGGTATGC 360
 101 K E C T F S C A S G E Y L E M K N Q V C 120
 361 AGTAAGTGTGCTGAAGGCACCTATTCTTGGGCAGTGGCATCAAATTTGATGAATGGGAT 420
 121 S K C G E G T Y S L G S G I K F D E W D 140
 421 GAATTGCCCGCAGGATTTCTAACATCGCAACATTCATGGACACTGTGGTGGGCGCTTCT 480
 141 E L P A G F S N I A T F M D T V V G P S 160
 481 GACAGCAGGCCAGACGGCTGTAACAACTCTTCTGGATCCCTCGTGGAAGTACATAGAA 540
 161 D S R P D G C N N S S W I P R G N Y I E 180
 541 TCTAATCGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC 600
 181 S N R D D C T V S L I Y A V H L K K S G 200
 601 TATGTCTTCTTTGAGTACCAGTATGTCGACAACAACATCTTCTTTGAGTTCTTTATTCAA 660
 201 Y V F F E Y Q Y V D N N I F F E F F I Q 220

FIG. 1A

661 AATGATCAGTGCCAGGAGATGGACACCACCCTGACAAGTGGGTAAACTTACAGACAAT 720
 221 N D Q C Q E M D T T T D K W V K L T D N 240
 721 GGAGAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA 780
 241 G E W G S H S V M L K S G T N I L Y W R 260
 781 ACTACAGGCATCCTTATGGGTCTAAGGCGGTCAAGCCTGTGCTGGTAAAAATATCACA 840
 261 T T G I L M G S K A V K P V L V K N I T 280
 841 ATTGAAGGGTGGCGTACACATCAGAATGTTTTCCTTGCAAGCCAGGCACATTCAGCAAC 900
 281 I E G V A Y T S E C F P C K P G T F S N 300
 901 AAACCAGGTTCAATTCAGTCCAGGTGTGTCCAGAAACACCTATTCTGAGAAAGGAGCC 960
 301 K P G S F N C Q V C P R N T Y S E K G A 320
 961 AAAGAATGTATAAGGTGTAAAGACGACTCTCAATTTTCAGGATCCAGTGAGTGACAGAG 1020
 321 K E C I R C K D D S Q F S G S S E C T E 340
 1021 CGCCCTCCCTGTACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA 1080
 341 R P P C T T K D Y F Q I H T P C D E E G 360
 1081 AAGACACACATAATGTACAAGTGGATAGAGCCCAAAATCTGCCGGGAGGATCTCACAGAT 1140
 361 K T Q I M Y K W I E P K I C R E D L T D 380
 1141 GCTATTAGATTGCCCCCTTCTGGAGAGAAGAAGGATTGTCCGCCCTTGCAACCCTGGATT 1200
 381 A I R L P P S G E K K D C P P C N P G F 400
 1201 TATAACAATGGATCATCTTCTTGCCATCCCTGTCTCTCTGGAACATTTTCAGATGGAACC 1260
 401 Y N N G S S S C H P C P P G T F S D G T 420
 1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTTGAATATAAATGG 1320
 421 K E C R P C P A G T E P A L G F E Y K W 440

FIG. 1B

1321 TGAATGTCCTTCCTGGCAACATGAAACTTCCTGCTTCAATGTTGGGAATTCAAAGTGC 1380
 441 W N V L P G N M K T S C F N V G N S K C 460
 1381 GATGGAATGAATGGTTGGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGGTTCT 1440
 461 D G M N G W E V A G D H I Q S G A G G S 480
 1441 GACAATGATTACCTGATCTTAACTTGCATATCCCAGGATTAAACCACCAACATCTATG 1500
 481 D N D Y L I L N L H I P G F K P P T S M 500
 1501 ACTGGAGCCACGGGTTCTGAAGTGAAGAATAACATTTGTCTTTGAGACCCTCTGTTCA 1560
 501 T G A T G S E L G R I T F V F E T L C S 520
 1561 GCTGACTGTGTTTTGTACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA 1620
 521 A D C V L Y F M V D I N R K S T N V V E 540
 1621 TCGTGGGGTGAACCAAAGAAAAACAAGCTTACACCCATATCATCTTCAAGAATGCAACT 1680
 541 S W G G T K E K Q A Y T H I I F K N A T 560
 1681 TTTACATTACATGGGCATTCCAGAGAACTAATCAGGGTCAAGATAATAGACGGTTCATC 1740
 561 F T F T W A F Q R T N Q G Q D N R R F I 580
 1741 AATGACATGGTGAAGATTTATTCTATCAGCCACTAATGCAGTTGATGGGGTGGCGTCC 1800
 581 N D M V K I Y S I T A T N A V D G V A S 600
 1801 TCATGCCGTGCCTGTGCCCTCGGTTCTGAACAGTCGGGTTTCATCGTGTGTCCTGCCCT 1860
 601 S C R A C A L G S E Q S G S S C V P C P 620
 1861 CCAGGCCACTACATTGAGAAAGAAACCAACCAGTGAACGAATGTCCACCTGACACCTAC 1920
 621 P G H Y I E K E T N Q C K E C P P D T Y 640
 1921 CTGTCCATACATCAGGTCTATGGCAAAGAGGCTTGTATTCCATGCGGGCCTGGGAGTAA 1980
 641 L S I H Q V Y G K E A C I P C G P G S K 660

FIG. 1C

1981 AACAAATCAGGACCATTCCGTTTGTATAGTGACTGCTTTTCTACCATGAAAAAGAAAAT 2040
 661 N N Q D H S V C Y S D C F F Y H E K E N 680
 2041 CAGATTTTGCACCTATGACTTTAGCAACCTCAGCAGTGTGGGCTCATTAAATGAATGGCCCC 2100
 681 Q I L H Y D F S N L S S V G S L M N G P 700
 2101 AGCTTCACCTCCAAAGGAACAAAATACTTCCATTCTTCAATATCAGTTTATGTGGGCAT 2160
 701 S F T S K G T K Y F H F F N I S L C G H 720
 2161 CAGGGGAAGAAGATGGCTCTCTGTACCAACAATATAACAGACTTTACAGTAAAAGAAATA 2220
 721 E G K K M A L C T N N I T D F T V K E I 740
 2221 GTGGCAGGGTCAGATGATTACACAAATTTGGTAGGGGCATTGTATGCCAGTCAACAATT 2280
 741 V A G S D D Y T N L V G A F V C Q S T I 760
 2281 ATTCCTTCTGAAAGTAAGGGTTTCCGAGCAGCCTTATCATCACAATCCATCATTCTGGCA 2340
 761 I P S E S K G F R A A L S S Q S I I L A 780
 2341 GATACATTCATAGCAGTCACAGTTGAAACCACATTGAAAAATATTAATATAAAAGAAGAT 2400
 781 D T F I G V T V E T T L K N I N I K E D 800
 2401 ATGTTCCCAGTTCCAACAAGCCAAATACCAGATGTGCATTCTTTTATAAGTCTTCTACA 2460
 801 M F P V P T S Q I P D V H F F Y K S S T 820
 2461 GCAACAACATCTTGTATTAATGGCCGATCAACTGCTGTGAAAATGAGGTGTAATCCTACT 2520
 821 A T T S C I N G R S T A V K M R C N P T 840
 2521 AAATCTGGAGCAGGAGTGATTTTCAGTCCCCAGCAAGTGGCCAGCAGGTACCTGTGATGGG 2580
 841 K S G A G V I S V P S K C P A G T C D G 860
 2581 TGTACGTTCTATTTCTGTGGGAGAGTGCTGAAGCTTGCCCTCTGTGTACGGAGCATGAC 2640
 861 C T F Y F L W E S A E A C P L C T E H D 880

FIG. 1D

1007333
 024300

2641 TTCCATGAGATTGAGGCAGCCTGCAAGAGAGGATTTGAGGAAACCTTGTATGTGTGGAAT 2700
881 F H E I E G A C K R G F Q E T L Y V W N 900

2701 GAACCTAAATGGTGCATTAAAGCAATTTCTTTGCCTGAGAAAAAGTTGGCAACCTGTGAA 2760
901 E P K W C I K G I S L P E K K L A T C E 920

2761 ACGGTTGACTTTTGGCTGAAGGTGGGAGCCGGTGTGGGAGCTTTTACTGCCGTTTGTCTG 2820
921 T V D F W L K V G A G V G A F T A V L L 940

2821 GTGGCTCTGACCTGCTACTTCTGAAAAAGAATCAAAAGAAAAAGAAGACCATTTTGAAT 2880
941 V A L T C Y F W K K N Q K K K K T I L N 960

2881 CTGTTCAACTGAAAACCTCAAGATCCCCAAATATATGAAGAGACAGTGTCTGTAGCCTTGA 2940
961 L F N * 964

2941 GACTAATGAACAAAGAAACCTGCTCTAGTTTTACAGGACCATATTTTAGGGTCTGTCTC 3000

3001 ATACCTGTACATTGGTGATCTCACAGAGGAGGCCATGCCGCTGAAAAGGGAAGGAGAT 3060

3061 TGAAACATTTGATTGCCTTATCACATGGTCAAGTACCTTGCCAAATAAAGGAAAGCAAAT 3120

3121 GATTTGGGTCTCAACTGAAGATGAAGCTCAACTCAGGAAGAGATTTATCTGTATATACAC 3180

3181 ATAACCTGAAAACCAAGTTTAAGCCCACCAATGCACTGCTGATGCATGCCATATAATTAAT 3240

3241 GGGTAACTTTTATTCTTTATGATGTCTACATAACAAGTGTGATTGGAAGGCACATGTGA 3300

3301 GCATATGCATTATGATCCAATTTATGTTTTTCTTTGTTTATATTTTGGGAAAATTAAA 3360

3361 ATTTTTTTAAGGTAAAAA 3390

FIG. 1E

FIG. 2A

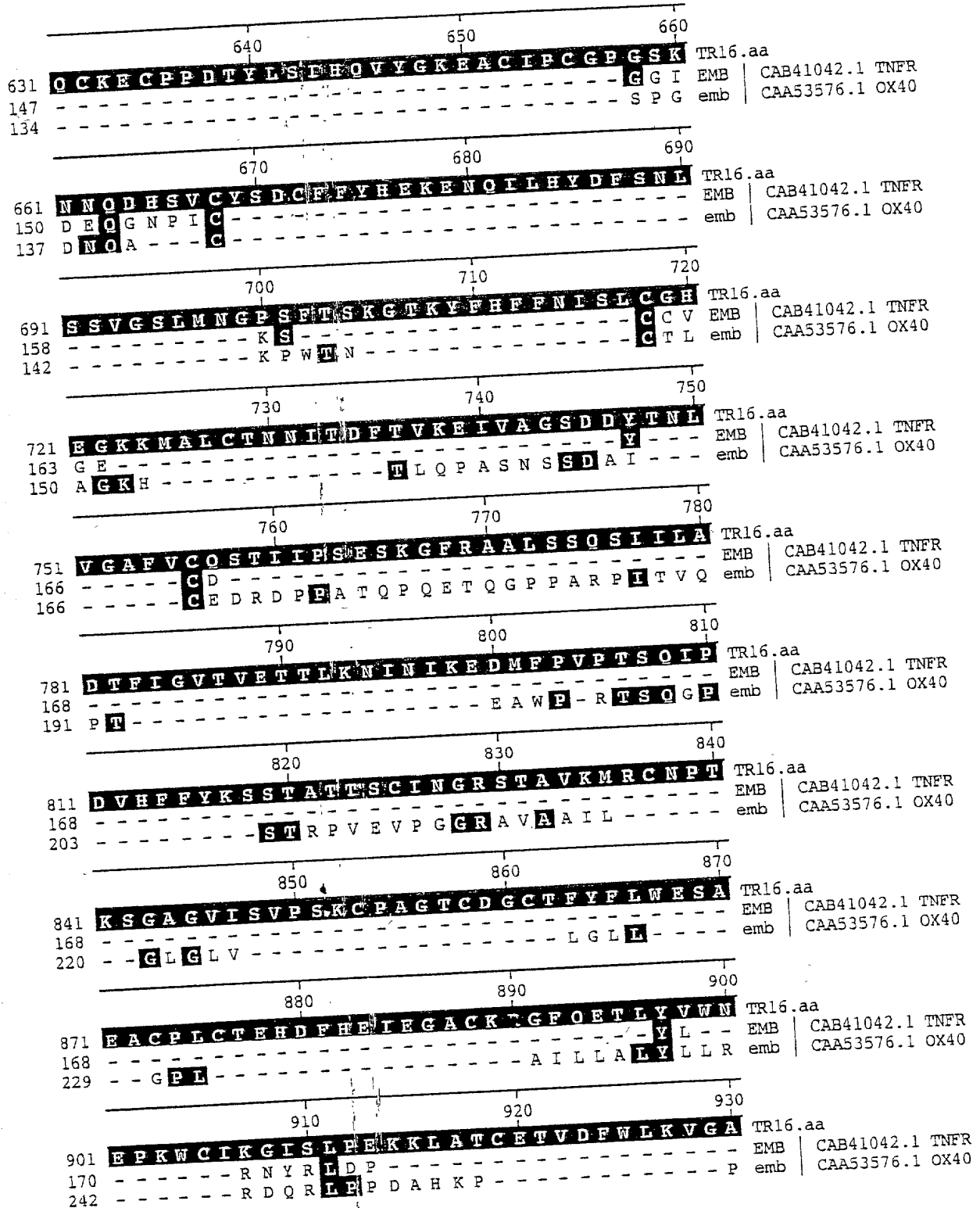
		10	20	30									
1		M L F R A R G P V R G R G V G R P A E A P R R G R S P F W S										TR16.aa	
1	M	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
1	M	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		40	50	60									
31		P A W I C C W A L A G C Q A A W A G D L P S S S S R P L P P										TR16.aa	
10	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
13	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		70	80	90									
61		C Q E K D Y H F E Y T E C D S S G S R W R V A I P N S A V D										TR16.aa	
23	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
26	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		100	110	120									
91		C S G L P D P V R G K E C T F S C A S G E Y L E M K N Q V C										TR16.aa	
30	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
31	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		130	140	150									
121		S K C G E G T Y S L G S G I K F D E W D E L P A G F S N I A										TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		160	170	180									
151		T F M D T V V G P S D S R P D G C N N S S W I P R G N Y I E										TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		190	200	210									
181		S N R D D C T V S L I Y A V H L K K S G Y V F F E Y Q Y V D										TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		220	230	240									
211		N N I F F E F F I Q N D Q C Q E M D T T T D K W V K L T D N										TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		250	260	270									
241		G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A										TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		280	290	300									
271		V K P V L V K N I T I E G V A Y T S E C F P C K P G T F S N										TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		310	320	330									
301		K P G S F N C O V C P R N T Y S E K G A K E C I R C K D D S										TR16.aa	
62	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
54	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40

202120" EEEF001

FIG. 2B

	340	350	360	
331	Q F S G S S E C T E R P P I C T T R D Y F Q I H T P C D E E G			TR16.aa
66	-			EMB CAB41042.1 TNFR
58	-			emb CAA53576.1 OX40
	370	380	390	
361	K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K			TR16.aa
66	-			EMB CAB41042.1 TNFR
58	-			emb CAA53576.1 OX40
	400	410	420	
391	K D C P P C N E G F Y N N G S S S C H P C P P G T F S D G T			TR16.aa
70	T K C E R C P B H T Y T A I P N Y S N G C - - - - -			EMB CAB41042.1 TNFR
62	T V C R P C G P G F Y N D V V S - S K P C - - - - -			emb CAA53576.1 OX40
	430	440	450	
421	K E C R P C P A G T E P A L G F E Y K W W N V L P G N M K T			TR16.aa
91	H Q C R K C - - P T G S - - - - - F D K V			EMB CAB41042.1 TNFR
82	K P C T W C N L R S G S - - - - - E R K Q			emb CAA53576.1 OX40
	460	470	480	
451	S C F N V G N S K C D G M N G W E V A G D H I Q S G A G G S			TR16.aa
105	K C T G T Q N S K C S C L P G W Y C A T D S S Q T - - - -			EMB CAB41042.1 TNFR
98	L C T A T Q D T V C R C R A G - - - - T Q P L D S - - - -			emb CAA53576.1 OX40
	490	500	510	
481	D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R			TR16.aa
130	-			EMB CAB41042.1 TNFR
119	-			emb CAA53576.1 OX40
	520	530	540	
511	I T E V F E T L C S A D C V L Y F M V D I N R K S T N V V E			TR16.aa
132	-			EMB CAB41042.1 TNFR
122	-			emb CAA53576.1 OX40
	550	560	570	
541	S W G G T K E K Q A Y T H I I P K N A T F T F T W A F O R T			TR16.aa
137	-			EMB CAB41042.1 TNFR
127	-			emb CAA53576.1 OX40
	580	590	600	
571	N O G O D N R R F I N D M V K I Y S I T A T N A V D G V A S			TR16.aa
137	-			EMB CAB41042.1 TNFR
127	-			emb CAA53576.1 OX40
	610	620	630	
601	S C R A C A L G S E Q S G S S C V P C P P G H Y I E K E T N			TR16.aa
141	-			EMB CAB41042.1 TNFR
128	-			emb CAA53576.1 OX40

FIG. 2C



202520" EEE2001

940 950 960

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TR16.aa
EMB | CAB41042.1 TNFR
emb | CAA53576.1 OX40

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TR16.aa

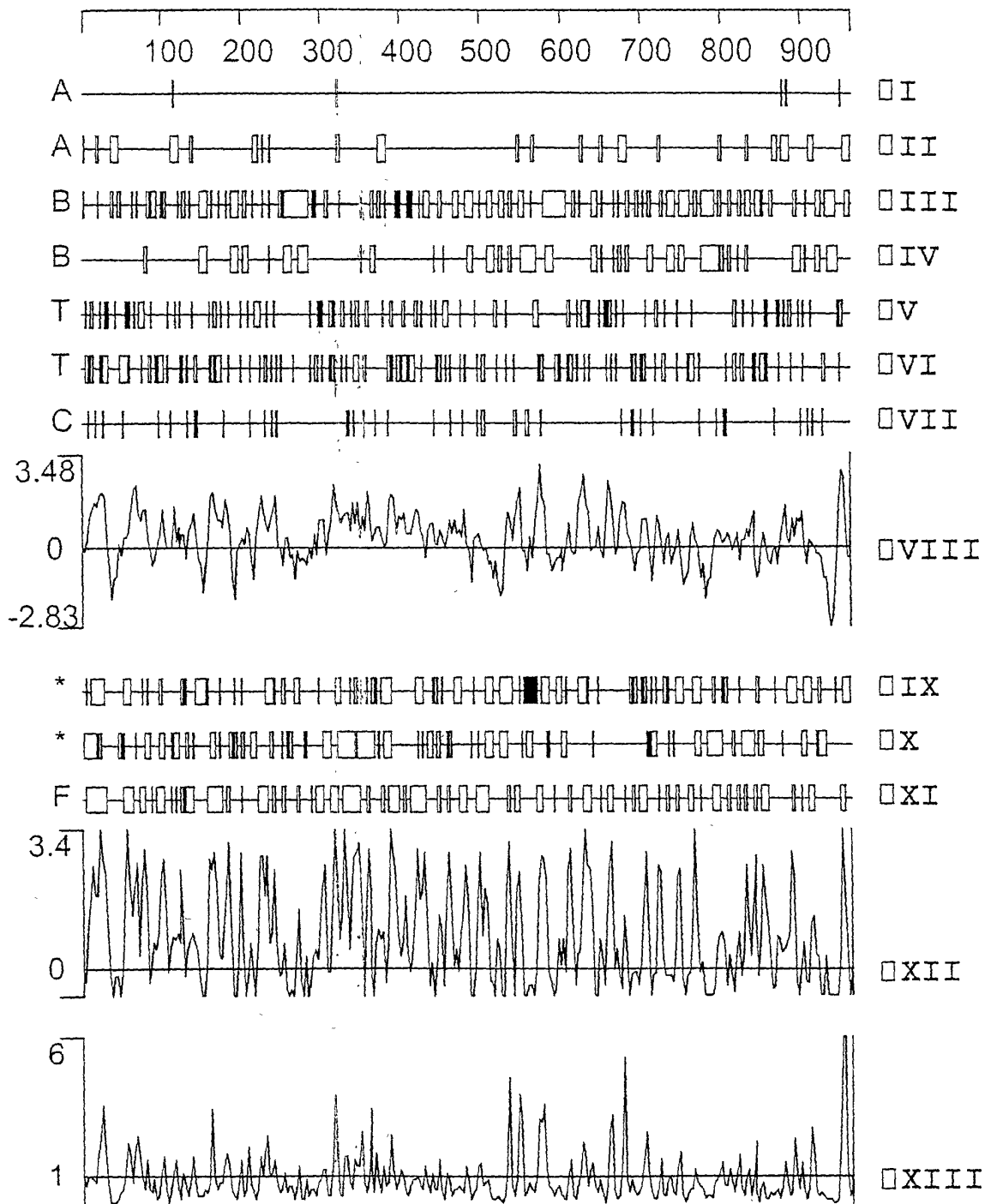


FIG. 3

1 ATGCTGTTCCGCCCCCGGGGCGGTACGGGGCAGGGGCTGGGGGCGGCGGAGGCT 60
 1 M L F R A R G P V R G R G W G R P A E A 20
 61 CCCCCCGCGGGGCTCGCCGCCCTGGAGCCCCGCCTGGATTGCTGCTGGGCGCTCGCC 120
 21 P R R G R S P P W S P A W I C C W A L A 40
 121 GGCTGCCAGGCGGCTGGGCTGGGACCTGCCCTCCTCCTCCAGCGCGCGCTTCCTCCT 180
 41 G C Q A A W A G D L P S S S S R P L P P 60
 181 TGCCAGGAGAAAGATTATCACTTTGAATATACGGAATGTGATAGCAGTGGCTCCAGGTGG 240
 61 C Q E K D Y H F E Y T E C D S S G S R W 80
 241 AGAGTTGCCATTCCAAATTCTGCACTGGACTGCTCTGCCCTGCCCTGACCCAGTGAGAGGC 300
 81 R V A I P N S A W D C S G L P D P V R G 100
 301 AAAGAATGCACTTTCTCCTGTCTCTGGAGAGTATCTAGAAATGAAGAACCAGGTATGC 360
 101 K E C T F S C A S G E Y L E M K N Q V C 120
 361 AGTAAGTGTGGTGAAGGCACCTATTCCTTGGGCAGTGGCATCAAATTTGATGAATGGGAT 420
 121 S K C G E G T Y S L G S G I K F D E W D 140
 421 GAATTGCCGGCAGGATTTTCTAACATCGCAACATTCATGGACACTGTGGTGGGCCCTTCT 480
 141 E L P A G F S N I A T F M D T V V G P S 160
 481 GACAGCAGGCCAGACGGCTGTAACAACTCTTCTTGGATCCCTCGTGGAAGTACATAGAA 540
 161 D S R P D G C N N S S W I P R G N Y I E 180
 541 TCTAATCGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC 600
 181 S N R D D C T V S L I Y A V H L K K S G 200
 601 TATGTCTTCTTTGAGTACCAGTATGTCGACAACAACATCTTCTTTGAGTTCTTTATTCAA 660
 201 Y V F F E Y Q Y V D N N I F F E F F I Q 220
 661 AATGATCAGTGCCAGGAGATGGACACCACCACTGACAAGTGGGTAAACTTACAGACAAT 720
 221 N D Q C Q E M D T T T D K W V K L T D N 240

FIG. 4A

721 GGAGAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA 780
 241 G E W G S H S V M L K S G T N I L Y W R 260
 781 ACTACAGGCATCCTTATGGGTTCTAAGGCGGTCAAGCCTGTGCTGGTAAAAATATCACA 840
 261 T T G I L M G S K A V K P V L V K N I T 280
 841 ATTGAAGGGGTGGCGTACACATCAGAATGTTTTCTTGCAAGCCAGGCACATTGAGCAAC 900
 281 I E G V A Y T S E C F P C K P G T F S N 300
 901 AAACCAGGTTTCATTCAACTGCCAGGTGTGTCCAGAAACACCTATTCTGAGAAAGGAGCC 960
 301 K P G S F N C Q V C P R N T Y S E K G A 320
 961 AAAGAATGTATAAGGTGTAAAGACGACTCTCAATTTTCAGGATCCAGTGAGTGACAGAG 1020
 321 K E C I R C K D D S Q F S G S S E C T E 340
 1021 CGCCCTCCCTGTACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA 1080
 341 R P P C T T K D Y F Q I H T P C D E E G 360
 1081 AAGACACAGATAATGTACAAGTGGATAGAGCCCAAAATCTGCCGGGAGGATCTCACAGAT 1140
 361 K T Q I M Y K W I E P K I C R E D L T D 380
 1141 GCTATTAGATTGCCCCCTTCTGGAGAGAAGAAGGATTGTCCGCCTTGCAACCCTGGATT 1200
 381 A I R L P P S G E K K D C P P C N P G F 400
 1201 TATAACAATGGATCATCTTCTTGCCATCCCTGTCTCCTGGAACATTTTCAGATGGAACC 1260
 401 Y N N G S S S C H P C P P G T F S D G T 420
 1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTTGAATATAAATGG 1320
 421 K E C R P C P A G T E P A L G F E Y K W 440
 1321 TGGAATGTCCTTCTGGCAACATGAAACTTCCTGCTTCAATGTTGGAATTCAAAGTGC 1380
 441 W N V L P G N M K T S C F N V G N S K C 460
 1381 GATGGAATGAATGGTTGGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGTTCT 1440
 461 D G M N G W E V A G D H I Q S G A G G S 480

FIG. 4B

1007333 02430
20120720 000000

1441 GACAATGATTACCTGATCTTAACTTGCATATCCCAGGATTAAACCACCAACATCTATG 1500
 481 D N D Y L I L N L H I P G F K P P T S M 500

1501 ACTGGAGCCACGGGTTCTGAACTAGGAAGAATAACATTTGTCTTTGAGACCCTCTGTTCA 1560
 501 T G A T G S E L G R I T F V F E T L C S 520

1561 GCTGACTGTGTTTTGTACTTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA 1620
 521 A D C V L Y F M V D I N R K S T N V V E 540

1621 TCGTGGGGTGGAAACAAAGAAAAACAAGCTTACACCCATATCATCTTCAAGAATGCAACT 1680
 541 S W G G T K E K Q A Y T H I I F K N A T 560

1681 TTTACATTTACATGGGCATTCCAGAGAACTAATCAGGGTCAAGATAATAGACGGTTCATC 1740
 561 F T F T W A F Q R T N Q G Q D N R R F I 580

1741 AATGACATGGTGAAGATTTATTCTATCACAGCCACTAATGCAGTTGATGGGGTGGCGTCC 1800
 581 N D M V K I Y S I T A T N A V D G V A S 600

1801 TCATGCCGTGCCTGTGCCCTCGTTCCTGAACAGTCCGGTTTCATCGTGTGCCCTGCCCT 1860
 601 S C R A C A L G S E Q S G S S C V P C P 620

1861 CCAGGCCACTACATTGAGAAAGAAACCAACCAGTGCAAGGAATGTCCACCTGACACCTAC 1920
 621 P G H Y I E K E T N Q C K E C P P D T Y 640

1921 CTGTCCATACATCAGGTCTATGGCAAAGAGGCTTGTATTCCATGCGGGCCTGGGAGTAAA 1980
 641 L S I H Q V Y G K E A C I P C G P G S K 660

1981 AACAAATCAGGACCATTGCGGTTTGCTATAGTGACTGCTTTTTCTACCATGAAAAAGAAAAT 2040
 661 N N Q D H S V C Y S D C F F Y H E K E N 680

2041 CAGATTTTGCACATGACTTTAGCAACCTCAGCAGTGTGGGCTCATTAATGAATGGCCCC 2100
 681 Q I L H Y D F S N L S S V G S L M N G P 700

2101 AGCTTCACCTCCAAAGGAACAAAATACTTCCATTTCTTCAATATCAGTTTATGTGGGCAT 2160
 701 S F T S K G T K Y F H F F N I S L C G H 720

FIG. 4C

2161 GAGGGGAAGAAGATGGCTCTCTGTACCAACAATATAACAGACTTTACAGTAAAAGAAATA 2220
721 E G K K M A L C T N N I T D F T V K E I 740

2221 GTGGCAGGGTCAGATGATTACACAAATTTGGTAGGGGCATTGTATGCCAGTCAACAATT 2280
741 V A G S D D Y T N L V G A F V C Q S T I 760

2281 ATTCCTTCTGAAAGTAAGGGTTTCCGAGCAGCCTTATCATCACAATCCATCATTCTGGCA 2340
761 I P S E S K G F R A A L S S Q S I I L A 780

2341 GATACATTCATAGGACTCACAGTTGAAACCACATTGAAAAATATTAATATAAAGAAGAT 2400
781 D T F I G V T V E T T L K N I N I K E D 800

2401 ATGTTCCAGTCCCAACAAGCCAAATACCAGATGTGCATTCTTTTATAAGTCTTCTACA 2460
801 M F P V P T S Q I P D V H F F Y K S S T 820

2461 GCAACAACATCTTGTATTAATGGCCGATCAACTGCTGTGAAATGAGGTGTAATCCTACT 2520
821 A T T S C I N G R S T A V K M R C N P T 840

2521 AAATCTGGAGCAGGACTGATTTTCAGTCCCCAGCAAGTCCCAGCAGGTACCTGTGATGGG 2580
841 K S G A G V I S V P S K C P A G T C D G 860

2581 TGTACGTTCTATTTCTGTGGGAGAGTGCTGAAGCTTCCCCTCTGTGTACCGAGCATGAC 2640
861 C T F Y F L W E S A E A C P L C T E H D 880

2641 TTCCATGACATTGAGGGAGCCTGCAAGAGAGGATTTGAGGAAACCTTGATGTGTGGAAT 2700
881 F H E I E G A C K R G F Q E T L Y V W N 900

2701 GAACCTAAATGGTGCATTAAAGGAATTTCTTTGCCTGAGAAAAAGTTGGCAACCTGTGAA 2760
901 E P K W C I K G I S L P E K K L A T C E 920

2761 ACGGTTGACTTTTGGCTGAAGGTGGGAGCCGGTGTGGGAGCTTTTACTGCCGTTTGTGCTG 2820
921 T V D F W L K V G A G V G A F T A V L L 940

2821 GTGGCTCTGACCTGCTACTTCTGGAAAAAGAATCAAAAAGTGAATACAAATATCCAAG 2880
941 V A L T C Y F W K K N Q K L E Y K Y S K 960

FIG. 4D

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2881 TTAGTAATGACGACTAACTCAAAAGACTGTGAACTCCCGGCTGCAGACAGTTGTGCTATC 2940
 961 L V M T T N S K E C E L P A A D S C A I 980
 2941 ATGGAAGGAGAAGATAATGAAGAGGAAGTTGTATATTCCAATAAACACTCACTACTAGGA 3000
 981 M E G E D N E E E V V Y S N K Q S L L G 1000
 3001 AAACCTCAAATCTTTGGCAACCAAGGAAAAAGAAGACCATTTTGAATCTGTTCAACTGAAA 3060
 1001 K L K S L A T K E K E D H F E S V Q L K 1020
 3061 ACCTCAAGATCCCCAAATATATGAAGAGACAGTGTGTAGCCTTGAGACTAATGAACAAA 3120
 1021 T S R S P N I * 1028
 3121 GAAACCTGCTCTAGTTTTACAGGACCATATTTAGGGTCTGTCTCATACCTGTCACATT 3180
 3181 GGTGATCTCAGAGGAGGGCCATGCCGCTGAAAAGGGAAGGAGATTGAAACATTTGATT 3240
 3241 GCCTTATCACATGGTCAAGTACCTTGCCAAATAAAGGAAAGCAAATGATTTGGGTCTCAA 3300
 3301 CTGAAGATGAAGCTCAACTCAGGAAGAGATTTATCTGTATATACACATAACTGAAAACCA 3360
 3361 AGTTTAAGCCCACCAATGCACTGCTGATGCATGCCATATAATTAATGGGTAACTTTATT 3420
 3421 CTTTATGATGTCTACATAACAAGTGTGATTTGGAAGGCACATGTGAGCATATGCATTATG 3480
 3481 ATCCAATTTATGTTTTTCTTTGTTTATATTTTGGGAAAATTAAAAATTTTTTAAGGTA 3540
 3541 AAAAAAAAAAAAAA 3556

FIG. 4E

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 021300

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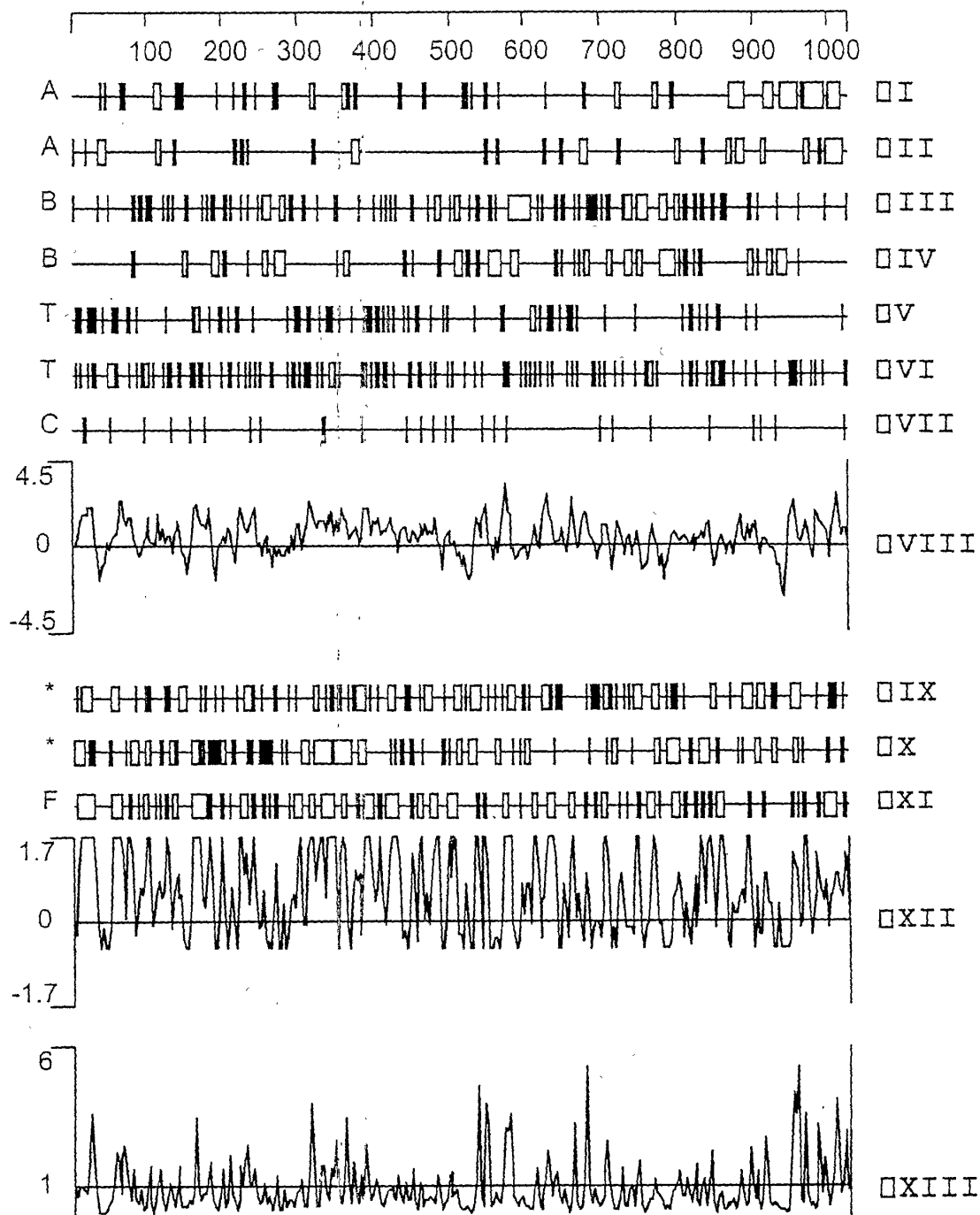


FIG. 5

		10	20	30	40	
1	1	MLFRARGPVRGRGWGRPAEAPRRGRSPPWSPA WICCWALA				SEQ ID 2
		-----				SEC10
		50	60	70	80	
41	1	GCQAAWAGDLPSSSSSRPLPPCQEKDYHFEYTECDSSGSRW				SEQ ID 2
		-----				SEC10
		90	100	110	120	
81	1	RVAIPNSAVDCSGLPDPVRGKECTFSCASGEYLE				SEQ ID 2
		-----MKNQVC				SEC10
		130	140	150	160	
121	7	SKCGEGTYSLGSGIKFDEWDELPAGFSNIATFMDTVVGPS				SEQ ID 2
		SKCGEGTYSLGSGIKFDEWDELPAGFSNIATFMDTVVGPS				SEC10
		170	180	190	200	
161	47	DSRPDGCNNSSWIPRGNYIESNRDDCTVSLIYAVHLKKS				SEQ ID 2
		DSRPDGCNNSSWIPRGNYIESNRDDCTVSLIYAVHLKKS				SEC10
		210	220	230	240	
201	87	YVFFEYQYVDNNIFFEFFIQNDQCQEMDTTTDKWVKLTDN				SEQ ID 2
		YVFFEYQYVDNNIFFEFFIQNDQCQEMDTTTDKWVKLTDN				SEC10
		250	260	270	280	
241	127	GEWGSHSVMLKSGTNILYWRRTTGILMGSKAVKPVLVKNIT				SEQ ID 2
		GEWGSHSVMLKSGTNILYWRRTTGILMGSKAVKPVLVKNIT				SEC10
		290	300	310	320	
281	167	IEGVAYTSECFCPKPGTFSENKPGSFNCQVCPRNTYSEKGA				SEQ ID 2
		IEGVAYTSECFCPKPGTFSENKPGSFNCQVCPRNTYSEKGA				SEC10
		330	340	350	360	
321	207	KECIRCKDDSQFS--GSSECTERPPCTTKDYFOIHTPCDE				SEQ ID 2
		KECIRCKDDSQFSEE GSSECTERPPCTTKDYFOIHTPCDE				SEC10
		370	380	390	400	
359	247	EGKTOIMYKWIEPKICREDLTDAILRLPPSGEKKDCPPCNP				SEQ ID 2
		EGKTOIMYKWIEPKICREDLTDAILRLPPSGEKKDCPPCNP				SEC10
		410	420	430	440	
399	287	GFYNNNGSSSCHPCPPGTFSDGTKECRPCPAGTEPALGFY				SEQ ID 2
		GFYNNNGSSSCHPCPPGTFSDGTKECRPCPAGTEPALGFY				SEC10
		450	460	470	480	
439	327	KWWNVLPGNMKTSCFNVGNSKCDGMNGWEVAGDHIQSGAG				SEQ ID 2
		KWWNVLPGNMKTSCFNVGNSKCDGMNGWEVAGDHIQSGAG				SEC10
		490	500	510	520	
479	367	GSDNDYLIILNLHIPGFKPPTSMTGATGSELGRITVFVETL				SEQ ID 2
		GSDNDYLIILNLHIPGFKPPTSMTGATGSELGRITVFVETL				SEC10

FIG. 6A

519	CSADCVLYFMVDINRKSTNVVESWGGTKEKQAYTHIIFKN	SEQ ID 2
407	CSADCVLYFMVDINRKSTNVVESWGGTKEKQAYTHIIFKN	SEC10
559	ATFTFTWAFQRTNQGGQDNRRFINDMVKIYSITATNAVDGV	SEQ ID 2
447	ATFTFTWGI PRE-----	SEC10
599	ASSCRACALGSEQSGSSCVPCPPGHYIEKETNQCKECPD	SEQ ID 2
459	-----	SEC10
639	TYLSIHQVYGKEACIPCGPGSKNNQDHSVCYSDCFFYHEK	SEQ ID 2
459	-----	SEC10
679	ENQILHYDFSNLSSVGS LMN GPSFTSKGTKYFHFNFNISLC	SEQ ID 2
459	----- LIQ GPR	SEC10
719	GHEGKKMALCTNNITDFTVKEIVAGSDDYTNLVGAFVCQS	SEQ ID 2
464	-----	SEC10
759	TIIPSESKGFRAALSSQSIILADTFIGVTVETTLKNINIK	SEQ ID 2
464	-----	SEC10
799	EDMFVPVPTSQIPDVHFFYKSSTATTSCTINGRSTAVKMRCN	SEQ ID 2
464	-----	SEC10
839	PTKSGAGVISVPSKCPAGTCDGCTFYFLWESAEACPLCTE	SEQ ID 2
464	-----	SEC10
879	HDFHEIEGACKRGFQETLYVWNEPKWCIKGISLPEKKLAT	SEQ ID 2
464	-----	SEC10
919	CETVDFWLKVGAGVGAF TAVLLVALTCYFWKKNQKKKKT I	SEQ ID 2
464	-----	SEC10
959	LNLFN	SEQ ID 2
464	-----	SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 6B

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		10	20	30	40	
1		MLFRARGPVRGRGWGRPAEAPRRGRSPPWSPA WICCWALA				SEQ ID 4
1		-----				SEC10
		50	60	70	80	
41		GCQAAWAGDLPSSSSSRPLPPCQEKDYHFEYTECDSSGSRW				SEQ ID 4
1		-----				SEC10
		90	100	110	120	
81		RVAIPNSAVDCSGLPDPVRGKECTFSCASGEYLEMKNQVC				SEQ ID 4
1		-----MKNQVC				SEC10
		130	140	150	160	
121		SKCGEGTYSLGSGIKFDEWDELPAGFSNIATFMDTVVGPS				SEQ ID 4
		SKCGEGTYSLGSGIKFDEWDELPAGFSNIATFMDTVVGPS				SEC10
		170	180	190	200	
161		DSRPDGCNNSSWIPRGNYIESNRDDCTVSLIYAVHLKKSG				SEQ ID 4
47		DSRPDGCNNSSWIPRGNYIESNRDDCTVSLIYAVHLKKSG				SEC10
		210	220	230	240	
201		YVFFFEYQYVDNNIFFEFFIQNDQCQEMDTTDDKWVKLTDN				SEQ ID 4
87		YVFFFEYQYVDNNIFFEFFIQNDQCQEMDTTDDKWVKLTDN				SEC10
		250	260	270	280	
241		GEWGSHSVMLKSGTNILYWRTTGILMGSKAVKPVLVKNIT				SEQ ID 4
127		GEWGSHSVMLKSGTNILYWRTTGILMGSKAVKPVLVKNIT				SEC10
		290	300	310	320	
281		IEGVAYTSECFPCPKPGTFSNKP GSFNCQVCP RNTYSEKGA				SEQ ID 4
167		IEGVAYTSECFPCPKPGTFSNKP GSFNCQVCP RNTYSEKGA				SEC10
		330	340	350	360	
321		KECIRCKDDSQFS--GSSECTERPPCTTKDYFQIH TPCDE				SEQ ID 4
207		KECIRCKDDSQFS EE GSSECTERPPCTTKDYFQIH TPCDE				SEC10
		370	380	390	400	
359		EGKTOIMYKWIEPKICREDLTDAIRLPPSGEKKDCPPCNP				SEQ ID 4
247		EGKTOIMYKWIEPKICREDLTDAIRLPPSGEKKDCPPCNP				SEC10
		410	420	430	440	
399		GFYNNGSSSCHPCPPGTFS DGTKECRPCPAGTEPALGFEY				SEQ ID 4
287		GFYNNGSSSCHPCPPGTFS DGTKECRPCPAGTEPALGFEY				SEC10
		450	460	470	480	
439		KWWNVLPGNMKTSCFNVGNSKCDGMNGWEVAGDHIQSGAG				SEQ ID 4
327		KWWNVLPGNMKTSCFNVGNSKCDGMNGWEVAGDHIQSGAG				SEC10
		490	500	510	520	
479		GSDNDYLILNLHIPGFKPPTSMTGATGSELGRITFVFETL				SEQ ID 4
367		GSDNDYLILNLHIPGFKPPTSMTGATGSELGRITFVFETL				SEC10

FIG. 7A

519	CSADCVLYFMVDINRKSTNVVESWGGTKEKQAYTHIIFKN	SEQ ID 4
407	CSADCVLYFMVDINRKSTNVVESWGGTKEKQAYTHIIFKN	SEC10
559	ATFTFTWAFQRTNQGDNRRFINDMVKIYSITATNAVDGV	SEQ ID 4
447	ATFTFTWGIPIRE-----	SEC10
599	ASSCRACALGSEQSGSSCVPCPPGHYIEKETNQCKECPD	SEQ ID 4
459	-----	SEC10
639	TYLSIHQVYGKEACIPCGPGSKNNQDHSVCSYDCFFYHEK	SEQ ID 4
459	-----	SEC10
679	ENQILHYDFSNLSSVGSIMNGPSFTSKGTYFHFNFNISLC	SEQ ID 4
459	-----LIQGP-----	SEC10
719	GHEGKKMALCTNNITDFTVKEIVAGSDDYTNLVGAFVCQS	SEQ ID 4
464	-----	SEC10
759	TIIPSESKGFRAALSSQSIILADTFIGVTVETTLKNINIK	SEQ ID 4
464	-----	SEC10
799	EDMFPVPTSQIPDVHFFYKSSSTATTSCTINGRSTAVKMRCN	SEQ ID 4
464	-----	SEC10
839	PTKSGAGVISVPSKCPAGTCDGCTFYFLWESAEACPLCTE	SEQ ID 4
464	-----	SEC10
879	HDFHEIEGACKRGRGFQETLYVWNEPKWCICKGISLPEKKLAT	SEQ ID 4
464	-----	SEC10
919	CETVDFWLKVGAGVGAFVALLVALTCYFWKKNQKLEYKY	SEQ ID 4
464	-----	SEC10
959	SKLVMTTNSKECELPAADSCAIMEGEDNEEEVVYSNKQSL	SEQ ID 4
464	-----	SEC10
999	LGKCLKSLATKEKEDHFESEVQLKTSRSPNI.	SEQ ID 4
464	-----R	SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 7B